

Input file T198sHVE1; Output File T198sHVE1.pat
Sequence length 1929

```

GTCGACCCACGCGTCCGCTCGGCTTTGCCTGGACAGCTCCTGCCTCCCGCAGGGCCACCTGTGTCCCCAGCGCCGCT 79
CCACCCAGCAGGCCTGAGCCCCCTCTCTGCTGCCAGACACCCCTGCTGCCACTCTCCTGTGCTCGGGTTCTGAGGCA 158
CAGCTTGTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCACAGCCGCAGCAATGGCGCTGAGTT 237
CCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCCGAGCTGCCGGTCTGAGCCTGAGGC M E P P G 5
ATG GAG CCT CCT GGA 311
D W G P P P W R S T P R T D V L R L V L 25
GAC TGG GGG CCT CCT CCC TGG AGA TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG 371
Y L T F L G A P C Y A P A L P S C K E D 45
TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC 431
E Y P V G S E C C P K C S P G Y R V K E 65
GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG 491
A C G E L T G T V C E P C P P G T Y I A 85
GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC 551
H L N G L S K C L Q C Q M C D P A M G L 105
CAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG 611
R A S R N C S R T E N A V C G C S P G H 125
CGC GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC 671
F C I V Q D G D H C A A C R A Y A T S S 145
TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC 731
P G Q R V Q K G G T E S Q D T L C Q N C 165
CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC 791
P P G T F S P N G T L E E C Q H Q T N R 185
CCC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAC CGA 851
A W K S Q T D L * 194
GCT TGG AAA AGT CAG ACA GAC CTC TGA 878
GGTCTCATCCTGGAGCTGCCACCAGCCAGCCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGG 957
CTCCCTGAGGCTGAGTGAACACTGGGCGCTGCACCTGCCTCTCCCACGTCCTCGGCCCACTCCCGCAGGTGCAGCTGG 1036
CTGGTGACGAAGGCCGGAGCTGGGACCAGCAGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCA 1115
TTGTTTGCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTC 1194
CATCCAGCGGAAAAAGACAGGAGGCAGAAAGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACG 1273
GTGGCCGTGGAGGAGACAATACCCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCC 1352
AGAGATACCTGGAGCGACGGCTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGAGGCTTGGGGGCTCC 1431
GCCCTGGGCTGGCTTCCGTCTCCTCCAGTGGAGGGAGAGGTGGGGCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGC 1510
CATTCCCATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCC 1589
AGTTGCCCTCGCTCACAGACCACACCCAGCCCTCCTGGGCCAGCCAGAGGGCCCTTCAGACCCAGCTGTCTGCG 1668
CGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTG 1747
TGGTGTTTAGTGATACCATCGGAAGTGATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTCTATTGTGTCATGA 1826
AACAGTGTATTTGGGGAGATGCTGTGGGAGGATGTAAATATCTTGTCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA 1905
AAAAAAAAAAAAAAAAAAAAAAAAA 1929

```

Figure 1

Cys
N-ly
out
in
ms

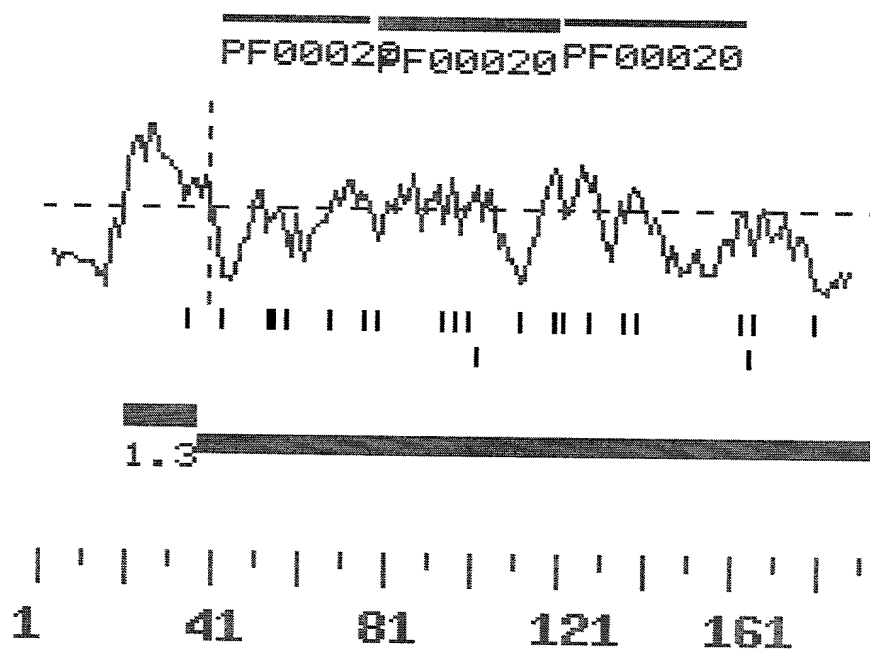


Figure 2

Input file T198sHVEM2; Output File T198sHVEM2.pat
Sequence length 1596

```

GTCGACCCACGCGTCCGGATGAAGGACCGCAGCAATGGCGCTGAGTTCTCTGCTGGAGTTCATCCTGCTAGCTGGGTT 79
      M   E   P   P   G   D   W   G   P   P   P   W   R   13
CCCAGCTGCCGGTCTGAGCCTGAGGC ATG GAG CCT CCT GGA GAC TGG GGG CCT CCT CCC TGG AGA 145
  S   T   P   R   T   D   V   L   R   L   V   L   Y   L   T   F   L   G   A   P   33
TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTT CTG GGA GCC CCC 205
  C   Y   A   P   A   L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   53
TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC 265
  C   P   K   C   S   P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   73
TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA 325
  V   C   E   P   C   P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   93
GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT 385
  L   Q   C   Q   M   C   D   P   A   M   G   L   R   A   S   R   N   C   S   R   113
CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG 445
  T   E   N   A   V   C   G   C   S   P   G   H   F   C   I   V   Q   D   G   D   133
ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC 505
  H   C   A   A   C   R   A   Y   A   T   S   S   P   G   Q   R   V   Q   K   G   153
CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA 565
  G   T   E   S   Q   D   T   L   C   Q   N   C   P   P   G   T   F   S   P   N   173
GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT 625
  G   T   L   E   E   C   Q   H   Q   T   N   W   P   N   H   M   C   E   K   K   193
GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAT TGG CCT AAT CAT ATG TGT GAA AAG AAG 685
  K   A   K   G   *
AAA GCC AAG GGG TGA 198
                                     700
GCACACGGCGGCCCCATCAGGGCTCATGTCCCAGCCGTCACCTCTTGAGCTCTGTACCCCCAAGCCTGGGAGGTGGC 779
CCCAGAGCTTTTCCAGGATCCGCGGCTCCTCCCAGGGCAGCCACTGCAGGCTGGGGCAGGTGATGTAGTCAAGGTGATC 858
GTCTCCATCCAGCGGAAAAGACAGGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCA 937
CCACGGTGGCCGTGGAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCG 1016
ACGCCAGAGATACCTGGAGCGACGGCTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGG 1095
GCTCCGCCCTGGGCTGGCTTCCGTCTCCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCA 1174
CGTGCCATTCCCATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGA 1253
GCGCCAGTTGCCCTCGCTCACAGACCACACCCAGCCCTCCTGGGCCAGCCAGAGGGCCCTTCAGACCCAGCTGT 1332
CTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTG 1411
CAGTGTGGTGTTTAGTGGATACCACATCGGAAGTGATTTTCTAAATTGGATTGGAATTCGGCTCCTGTTTTCTATTTGT 1490
CATGAAACAGTGTATTTGGGGAGATGCTGTGGGAGGATGTAAATATCTTGTTCCTCAAAAAAAAAAAAAAAAAAAAA 1569
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA
                                     1596

```

Figure 3

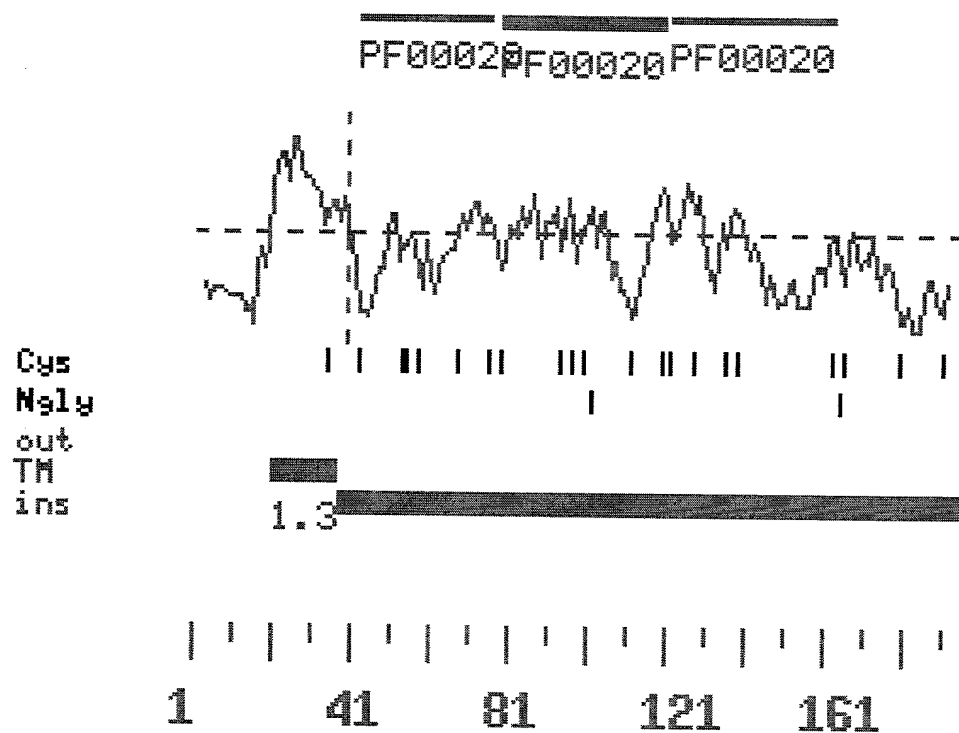


Figure 4

Input file sHVEM3; Output File sHVEM3.pat
Sequence length 2313

```

GTCGACCCACGCGTCCGGCTGAGTTCCTCTGCTGGAGTTCATCTCTGCTAGCTGGGTTCCTCCGAGCTGCCGGTCTGAGCCT 79

      M   E   P   P   G   D   W   G   P   P   P   W   R   S   T   P   R   T      18
GAGGC ATG GAG CCT CCT GGA GAC TGG GGG CCT CCT CCC TGG AGA TCC ACC CCC AGA ACC      138

      D   V   S   R   L   V   L   Y   L   T   F   L   G   A   P   C   Y   A   P   A      38
GAC GTC TCG AGG CTG GTG CTG TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT      198

      L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   C   P   K   C   S      58
CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT      258

      P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   V   C   E   P   C      78
CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC      318

      P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   L   Q   C   Q   M      98
CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG      378

      C   D   P   A   M   G   L   R   A   S   R   N   C   S   R   T   E   N   A   V      118
TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG      438

      C   G   C   S   P   G   H   F   C   I   V   Q   D   G   D   H   C   A   A   C      138
TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC      498

      R   A   Y   A   T   S   S   P   G   Q   R   V   Q   K   G   G   T   E   S   Q      158
CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG      558

      D   T   L   C   Q   N   C   P   P   G   T   F   S   P   N   G   T   L   E   E      178
GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA      618

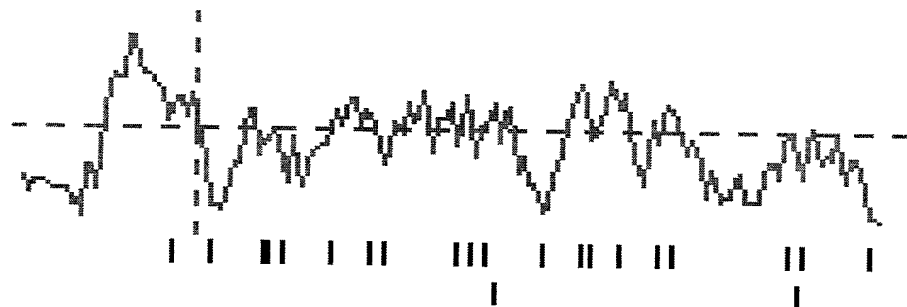
      C   Q   H   Q   T   K   K   A   *
TGT CAG CAC CAG ACC AAA AAG GCT TGA      187
                                           645

AGGTCACCCACCTGAGCGGCACCTTGGTCACATGCCTGCGTCCAGGAGAGCTGCAGGGCTGAAGCCTGTGTGCCCCAGAT 724
AACCCCTTCCATGGGCCCAGACAAAGCCTCATCAGATCTGAGCTTCTGAGGGCTCAGGATGGGCTTCCCAGAAGCAG 803
GCCAGAGGGAGGCTGCCTCCAGATCCCCCTGTCCCTGGGGCTGTGGGTGTCCCTGAATGTGAGGGCCATGGGAGGGCC 882
CCTGGGCTTCAGGGGTGGGGAAAGTGAACACTCTGCTCTTTGTCCACCTTCGGGAGGACACCTTCAAATGCTGACCCT 961
GGGCCCCTAACCTGACCTGAGACTTCAGAGCTTCTTGGGAGGAGCTGGGGTCCCCAGCGGAGCCTGGGATGGAGCAGGG 1040
ATGGCTGCCCCAGGGAGGGGGCGGTGGGGCTTCCATCCTGCTCTGCCCTCCTCGTCTCTGCCCCAGCTCAGTCTCTG 1119
TCCATCTCCAGCTCTAACCATTTTTGTCCCCGACACTGGCTCTCCCTCTACCTTCTGTCCTTGTCTGCCACTGGTCTCCC 1198
GTGCTCTGGGGTCTCTGCACTGCTGGCTGCCTCCCGCTTCTCTCCCTCTCCCTCTGCCGTCTGTCTCTCTTTGCCAG 1277
TCTCTCCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1356
AGGTCTCATCTGAGCTGCCACCAGCCAGCCTCCCTGGGACCTGCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAG 1435
GCTCCCTGAGGCTGAGTGAACACTGGGCGCTGCACCTGCCTCTCCACGTCTCGGCCCCACTCCCGCAGGTGCAGCTG 1514
GCTGGTGACGAAGGCCGAGCTGGGACACAGCCTCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTC 1593
ATTGTTTGTCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGCAAGGGGTGATGTAGTCAAGGTGATCGTCT 1672
CCGTCCAGCGGAAAAGACAGGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCAACCAC 1751
GGTGGCCGTGGAGGAGACAATACCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGC 1830
CAGAGATACCTGGAGCGACGCTGCTGAAAGAGGCTGCCACCTGGCGAAACCACCGAGCCCGAGGCTTGGGGGCTC 1909
CGCCCTGGGCTGGCTTCCGTCTCCTCCAGTGGAGGGAGAGGTGGGGCCCTGCTGGGGTAGAGCTGGGGACGCCACGTG 1988
CCATTCATGGGCGAGTGGGGCTTGGGGCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTCTGAGGAGGAGCGC 2067
CAGTTGCCCCCTCGCTCACAGACACACACCCAGCCCTCTGGGCGAGCCAGAGGGCCCTTCCAGACCCAGCTGTCTGC 2146
GCGTCTGACTCTGTGGCCTCAGCAGGACAGGCCCGGGCAGTGCCTCACAGCCAAGGCTGAGCTGGGTGGCTGTCAGT 2225
GTGGTGTTTAGTGGATACCATCGGAAGTGATTTTCTAAATTGGATTGTAATTCGGAACCAAGGCTGGGTTGGCTGTCAGT 2304
GGCGGCCCGC
                                           2313

```

Figure 5

PF00020 PF00020 PF00020



Cgs
Nsl
out
TN
ins

2.2

1 41 81 121 161

Figure 6

GTCGACCCACGCGTCCGCACAGCCGAGCAATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCCG 79
 M E P P G D W G P P P W R S 14
 AGCTGCCGGTCTGAGCCTGAGGC ATG GAG CCT CCT GGA GAC TGG GGG CCT CCT CCC TGG AGA TCC 144
 T P R T D V L R L V L Y L T F L G A P C 34
 ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTC CTG GGA GCC CCC TGC 204
 Y A P A L P S C K E D E Y P V G S E C C 54
 TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC 264
 P K C S P G Y R V K E A C G E L T G T V 74
 CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA GTG 324
 C E P C P P G T Y I A H L N G L S K C L 94
 TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT CTG 384
 Q C Q M C D P A M G L R A S R N C S R T 114
 CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG ACA 444
 E N A V C G C S P G H F C I V Q D G D H 134
 GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC CAC 504
 C A A C R A Y A T S S P G Q R V Q K G G 154
 TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC 564
 T E S Q D T L C Q N C P P G T F S P N G 174
 ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT GGG 624
 T L E E C Q H Q T K C S W L V T K A G A 194
 ACC CTG GAG GAA TGT CAG CAC CAG ACC AAG TGC AGC TGG CTG GTG ACG AAG GCC GGA GCT 684
 G T S S S H W V W W F L S G S L V I V I 214
 GGG ACC AGC AGC TCC CAC TGG GTA TGG TGG TTT CTC TCA GGG AGC CTC GTC ATC GTC ATT 744
 V C S T V G L I I C V K R R K P R G D V 234
 GTT TGC TCC ACA GTT GGC CTA ATC ATA TGT GTG AAA AGA AGA AAG CCA AGG GGT GAT GTA 804
 V K V I V S V Q V L I L L P L S L P P P 254
 GTC AAG GTG ATC GTC TCC GTC CAG GTA TTG ATC CTC CTC CCC CTC TCC CTC CCC CCT CCA 864
 P S H L P S P R W G W C F W C T W W G L 274
 CCT TCC CAC CTC CCC TCT CCC CGC TGG GGC TGG TGT TTC TGG TGT ACA TGG TGG GGG CTC 924
 P V L * 278
 CCA GTT CTC TGA 936
 GGGTCCTGAGTCTTTCAAGTACAGCCACGGTAGCTCAGGAAAGAACCCACCCCTCAAACCTGAAAGCAGTAAATGAAC 1015
 CCGAGAACCTGGAGTCCCAGGGGGGCTGAGCAGGCAGGGTCTCCACGATTCTGTGTGCTCACAGCGGAAAAGACAGGAG 1094
 GCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGACGTACCACGGTGGCCGTGGAGGAGACAATAC 1173
 CCTCATTACGGGGAGGAGCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGGCT 1252
 GCTGAAAGAGGCTGTCCACTGGCGAAACACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCTC 1331
 CTCCAGTGGAGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG 1410
 CCTGGGGCCTCTGTCTGTGTGGCCTGAGCTCCCCAGAGTCCCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACC 1489
 ACACACCCAGCCCTCTGGGCCAGCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAG 1568
 CAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTGTTAGTGGATACCACAT 1647
 CGGAAGTGATTTTCTAAATTTGATTTGAATTCGGCTCCTGTTTTCTATTTGTATGAAACAGTGTATTTGGGGAGATGC 1726
 TGTGGGAGGATGTAAATATCTTGTCTCTCTCAA 1805
 AAAAAAAAAAAAAAAAAAAGGGCGGCCGC 1834

Figure 7

Cys
N-gly
out
TH
ins

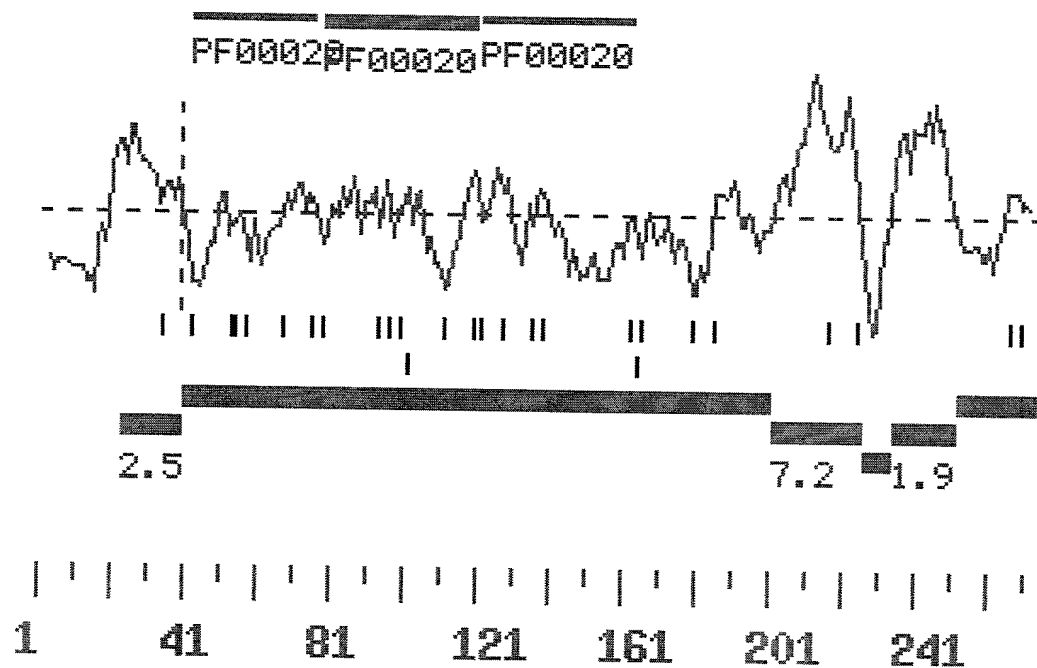


Figure 8

SHVEM_1_n.a. 1521
 SHVEM_2_n.a. -----CGAGCTTGGAAAAGTCAGACAGACCTCTGAGGTCTCATCCTGGAGCTGCCACAGCCC
 SHVEM_3_n.a. -----
 mHVEM_2_n.a. CTTCTCTCCACCTCCCCATAGCCGAGCTTGGAAAAGTCAGACAGACCTCTGAGGTCTCATCCTGGAGCTGCCACAGCCC
 mHVEM_pub._n.a. -----

SHVEM_1_n.a. 1601
 SHVEM_2_n.a. AGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGC
 SHVEM_3_n.a. -----
 mHVEM_2_n.a. AGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGC
 mHVEM_pub._n.a. -----G-----G-----

SHVEM_1_n.a. 1681
 SHVEM_2_n.a. TGCACCTGCCTCTCCACGTCTCGGCCCACTCCCGCAGGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC
 SHVEM_3_n.a. -----
 mHVEM_2_n.a. TGCACCTGCCTCTCCACGTCTCGGCCCACTCCCGCAGGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC
 mHVEM_pub._n.a. -----TGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC

SHVEM_1_n.a. 1761
 SHVEM_2_n.a. AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG
 SHVEM_3_n.a. -----TTG-----GCCTAATCATATG
 mHVEM_2_n.a. AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG
 mHVEM_pub._n.a. AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG

SHVEM_1_n.a. 1841
 SHVEM_2_n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC-----
 SHVEM_3_n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC-----
 mHVEM_2_n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC-----
 mHVEM_pub._n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC-----

SHVEM_1_n.a. 1920
 SHVEM_2_n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC-----
 SHVEM_3_n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC-----
 mHVEM_2_n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC-----
 mHVEM_pub._n.a. TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC-----

SHVEM_1_n.a. 2000
 SHVEM_2_n.a. TCACCTCTTGG-----AGCTCTG-TCACCCCAA-----GCCTGG-----GAGGTGGC-CCCAGAGCTT
 SHVEM_3_n.a. -----
 mHVEM_2_n.a. TCACCTCTTGG-----AGCTCTG-TCACCCCAA-----GCCTGG-----GAGGTGGC-CCCAGAGCTT
 mHVEM_pub._n.a. TCCCCCTCCACCTTCCACCTCCCTCTCCCCGCTGGGGCTGGTGTCTTCTGGTGTACATGGTGGGGCTCCAGTTCTC

SHVEM_1_n.a. 2001
 SHVEM_2_n.a. TTCCAGGATCCGCGGCTCCTCCAGGGCAGCCACTG-----CAGG-----CTGGG-GCAGG-----
 SHVEM_3_n.a. -----
 mHVEM_2_n.a. TG--AGGGTCTGAG-TCTTTCAAGTACAGCCACGGTAGCTCAGGAAAGAACCCACCCCTCAAACCTGAAAGCAGTAAAA
 mHVEM_pub._n.a. -----

SHVEM_1_n.a. 2081
 SHVEM_2_n.a. TGA-----TGATGTC--AAGG-----TGATC-----G-TCTCCA-----CAGCGGAAAAGACA
 SHVEM_3_n.a. -----
 mHVEM_2_n.a. TGAACCCGAGAACCTGGAGTCCCAGGGGGCCTGAGCAGGCAGGGTCTCCACGATTCGTGTGCTCAGCGGAAAAGACA
 mHVEM_pub._n.a. -----CAGCGGAAAAGACA

SHVEM_1_n.a. 2161
 SHVEM_2_n.a. GGAGGCAGAAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCAACACGGTGGCCGTGGAGGAGACAA
 SHVEM_3_n.a. GGAGGCAGAAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCAACACGGTGGCCGTGGAGGAGACAA
 mHVEM_2_n.a. GGAGGCAGAAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCAACACGGTGGCCGTGGAGGAGACAA
 mHVEM_pub._n.a. GGAGGCAGAAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCAACACGGTGGCCGTGGAGGAGACAA

SHVEM_1_n.a. 2240
 SHVEM_2_n.a. GGAGGCAGAAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCAACACGGTGGCCGTGGAGGAGACAA
 SHVEM_3_n.a. GGAGGCAGAAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCAACACGGTGGCCGTGGAGGAGACAA
 mHVEM_2_n.a. GGAGGCAGAAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCAACACGGTGGCCGTGGAGGAGACAA
 mHVEM_pub._n.a. GGAGGCAGAAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCCTCCGGACGTCAACACGGTGGCCGTGGAGGAGACAA

Figure 9C

shVEM_1_n.a.	2241	TACCCCTCATTACGGGGAGGAGCCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG	2320
shVEM_2_n.a.		TACCCCTCATTACGGGGAGGAGCCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG	
shVEM_3_n.a.		TACCCCTCATTACGGGGAGGAGCCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG	
mHVEM_2_n.a.		TACCCCTCATTACGGGGAGGAGCCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG	
mHVEM_pub._n.a.		TACCCCTCATTACGGGGAGGAGCCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGG	
shVEM_1_n.a.	2321	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	2400
shVEM_2_n.a.		CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
shVEM_3_n.a.		CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
mHVEM_2_n.a.		CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
mHVEM_pub._n.a.		CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
shVEM_1_n.a.	2401	CCTCCAGTGGAGGGAGAGGTGGGGCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	2480
shVEM_2_n.a.		CCTCCAGTGGAGGGAGAGGTGGGGCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
shVEM_3_n.a.		CCTCCAGTGGAGGGAGAGGTGGGGCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
mHVEM_2_n.a.		CCTCCAGTGGAGGGAGAGGTGGGGCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
mHVEM_pub._n.a.		CCTCCAGTGGAGGGAGAGGTGGGGCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
shVEM_1_n.a.	2401	CCTGGGGCCTCTGTTCTGCTGTGGCTGAGCTCCCCAGAGTCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	2560
shVEM_2_n.a.		CCTGGGGCCTCTGTTCTGCTGTGGCTGAGCTCCCCAGAGTCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
shVEM_3_n.a.		CCTGGGGCCTCTGTTCTGCTGTGGCTGAGCTCCCCAGAGTCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
mHVEM_2_n.a.		CCTGGGGCCTCTGTTCTGCTGTGGCTGAGCTCCCCAGAGTCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
mHVEM_pub._n.a.		CCTGGGGCCTCTGTTCTGCTGTGGCTGAGCTCCCCAGAGTCTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
shVEM_1_n.a.	2561	CACACCCAGCCCTCCTGGGCCAGCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	2640
shVEM_2_n.a.		CACACCCAGCCCTCCTGGGCCAGCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
shVEM_3_n.a.		CACACCCAGCCCTCCTGGGCCAGCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
mHVEM_2_n.a.		CACACCCAGCCCTCCTGGGCCAGCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
mHVEM_pub._n.a.		CACACCCAGCCCTCCTGGGCCAGCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
shVEM_1_n.a.	2641	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTATTAGTGGATACCACATCGG	2720
shVEM_2_n.a.		GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTATTAGTGGATACCACATCGG	
shVEM_3_n.a.		GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTATTAGTGGATACCACATCGG	
mHVEM_2_n.a.		GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTATTAGTGGATACCACATCGG	
mHVEM_pub._n.a.		GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTATTAGTGGATACCACATCGG	
shVEM_1_n.a.	2721	AAGTGATTTTCTAAATTGGATTGGAATTCCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGGGGAGATGCTGTG	2800
shVEM_2_n.a.		AAGTGATTTTCTAAATTGGATTGGAATTCCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGGGGAGATGCTGTG	
shVEM_3_n.a.		AAGTGATTTTCTAAATTGGATTGGAATTCCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGGGGAGATGCTGTG	
mHVEM_2_n.a.		AAGTGATTTTCTAAATTGGATTGGAATTCCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGGGGAGATGCTGTG	
mHVEM_pub._n.a.		AAGTGATTTTCTAAATTGGATTGGAATTCCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGGGGAGATGCTGTG	
shVEM_1_n.a.	2801	GGAGGATGTAAATATCTTGTCTCTCAA	2880
shVEM_2_n.a.		GGAGGATGTAAATATCTTGTCTCTCAA	
shVEM_3_n.a.		GGAGGATGTAAATATCTTGTCTCTCAA	
mHVEM_2_n.a.		GGAGGATGTAAATATCTTGTCTCTCAA	
mHVEM_pub._n.a.		GGAGGATGTAAATATCTTGTCTCTCAA	
shVEM_1_n.a.	2881	-----	2904
shVEM_2_n.a.		-----	
shVEM_3_n.a.		-----GGGCGGCCCGC	
mHVEM_2_n.a.		AAAAAAAAAAAAAAAAAGGCGGCCCGC	
mHVEM_pub._n.a.		-----	

Figure 9D

shVEM_1_a.a.	1	MEPPGDWGPWPWRSTPRTDVLRLVLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	80
shVEM_2_a.a.		MEPPGDWGPWPWRSTPRTDVLRLVLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
shVEM_3_a.a.		MEPPGDWGPWPWRSTPRTDVLRLVLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
mHVEM_2_a.a.		MEPPGDWGPWPWRSTPRTDVLRLVLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
mHVEM__pub.__a.a.		MEPPGDWGPWPWRSTPRTDVLRLVLVLYLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
shVEM_1_a.a.	81	GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQVRVQKGGTESQDT	160
shVEM_2_a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQVRVQKGGTESQDT	
shVEM_3_a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQVRVQKGGTESQDT	
mHVEM_2_a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQVRVQKGGTESQDT	
mHVEM__pub.__a.a.		GTYIAHLNGLSKCLQCQMCDPAMGLRASRNCSTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQVRVQKGGTESQDT	
shVEM_1_a.a.	161	LCQNCPPGTFSPNGTLEECQHQTNRWKSQTDL-----	240
shVEM_2_a.a.		LCQNCPPGTFSPNGTLEECQHQTNRWPNHMCEKKKAG-----	
shVEM_3_a.a.		LCQNCPPGTFSPNGTLEECQHQTTKA-----	
mHVEM_2_a.a.		LCQNCPPGTFSPNGTLEECQHQTCSWLVTKAGAGTSSSHWVWVFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS	
mHVEM__pub.__a.a.		LCQNCPPGTFSPNGTLEECQHQTCSWLVTKAGAGTSSSHWVWVFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS	
shVEM_1_a.a.	241	-----	283
shVEM_2_a.a.		-----	
shVEM_3_a.a.		-----	
mHVEM_2_a.a.		VQVLILPLSLPPPPSHLPSPRWGWCFCWTWWGLPVL-----	
mHVEM__pub.__a.a.		VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH	

Figure 10